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 searching Seq1 library
 Comparison of:
(A) AE015579   >AE015579  (681 nucleotides)                  – 681 nt
(B) Seq1       >Seq1  (678 nucleotides)                      – 678 nt
 using matrix file DNA

  75.7% identity in 678 nt overlap; init: 1548, opt: 1557


               10        20        30        40        50        60
AE0155 ATGGAACCGATTAAAAATTTGCCTCGTCTGTGTCGTACGTTGGGGTATGAGTTCAAGAAT
       X::::::: ::::::::::::: ::: :::: ::::: :: :: ::::::::::: :::
Seq1   ATGGAACCCATTAAAAATTTGCCGCGTTTGTGCCGTACTTTAGGTTATGAGTTCAATAAT
               10        20        30        40        50        60


               70        80        90       100       110       120
AE0155 CTTGACCTTCTAACCCAAGCGTTGACCCATAGAAGTGCGGCAAATAAGCACAATGAACGT
        ::::  : :: :  :: :: :: :: ::: : :: :: :::::::: :: ::::: :::
Seq1   ATTGAATTACTTATTCAGGCCTTAACACATCGTAGCGCAGCAAATAAACATAATGAGCGT
               70        80        90       100       110       120


              130       140       150       160       170       180
AE0155 TTAGAGTTTTTAGGCGATTCAATTTTATCGATTGTGATTTCAGACGCCTTATATCATCAG
       :::::::::::::::: ::::: :::::::::: :  ::::::::: ::::::::::::::::
Seq1   TTAGAGTTTTTAGGTGATTCGATTTTATCGATAGCCATTTCAGATGCCTTATATCATCAG
               130       140       150       160       170       180


              190       200       210       220       230       240
AE0155 TTTCCTAAGGCGACTGAGGGTGATTTGAGCCGGATGCGCGCCACCTTAGTACGCGGTGAT
       ::::: :::::::::::: :::::::: ::::: :::::::::::: :::::   :::::
Seq1   TTTCCAAAGGCGACTGAAGGTGATTTAAGCCGAATGCGCGCCACTTTAGTCAAAGGTGAC
               190       200       210       220       230       240


              250       260       270       280       290       300
AE0155 ACGCTCACCTTGATTGCTCAAGCATTTAAGCTCGGGGATTATTTATTTTTAGGCCCTGGC
       ::::: ::   : :: ::: :::   :: ::::: :::::: :: ::::: : ::::: ::
Seq1   ACGCTGACAATCATAGCTAAAGAGTTCAAGCTAGGTGATTATTTGTATTTAGGTCCTGGT
               250       260       270       280       290       300


              310       320       330       340       350       360
AE0155 GAGTTAAAGAGTGGTGGTTTTAGGCGCGAGTCGATTCTGGCCGATGCGGTCGAGGCGATT
       ::  : :: :::::::::: :::::: ::::: ::::: :: ::: : :: ::::: :: :: :::
Seq1   GAACTCAAAAGTGGTGGCTTTAGACGCGAATCTATTTTAGCTGATGCTGTAGAGGCTATT
               310       320       330       340       350       360


              370       380       390       400       410       420
AE0155 ATCGGGGCAATTTACTTAGATTCCGACCTCGAAGTGTGCCGTCAGTTGTTGCTTAATTGG
       :: :: :: : :: ::: : :  : :::::::::::: :: :::  :: :::::      :::
Seq1   ATTGGTGCTGTCTATCTTGATGCTGATATTGAAGTGTGCCGCAAGCTATTATTATCATGG
               370       380       390       400       410       420


              430       440       450       460       470       480
AE0155 TACGCCGAGCGTTTGGCTGAGATCCAACCCGGTATTAATCAAAAAGACGCTAAAACCTTA
       ::     :::::::: ::::::::: :::: :::::::::::::::::: : :: :: ::
Seq1   TATCAAGAGCGTTTAGCTGAGATTAAACCGGGTATTAATCAAAAAGATCCGAAGACAATA
               430       440       450       460       470       480


              490       500       510       520       530       540
AE0155 CTGCAAGAATATTTACAAGGGTTAAAGAAGCCGCTACCCGATTACCAAGTAATCAATATA
        :::::::::: : ::::: :: :: ::::: : :: :::::::::::::: :       ::
Seq1   TTGCAAGAATACCTGCAAGGTTTTAAAAAGCCATTGCCTGATTACCAAGTTGTTGCAGTA
               490       500       510       520       530       540


              550       560       570       580       590       600
AE0155 GAAGGCGATGCCCACGATCAAACATTCACTGTTGAATGTCGTATAGATGACTTGAGCCAA
       ::::: :: :::::: :::::::: ::::: :::::: :: ::    ::: ::       ::
Seq1   GAAGGTGAAGCCCATGATCAAACCTTCACCGTAGAATGTAAAATTAGTGAATTAGATAAA
               490       500       510       520       530       540
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             550        560        570        580        590        600


             610        620        630        640        650        660
AE0155 AGCGTGATAGGTGTAGCGAGTTCGCGCCGCAAAGCCGAGCAAATTGCCGCCGCTCAAGTA
          :: :   :::::: ::  :::::  :   : :::::  :: ::  ::::::: ::::: :::
Seq1   GTTGTCACCGGTGTGGCAAGTTCAAGAAGAAAAGCTGAACAGCTTGCCGCTGCTCAGGTA
             610        620        630        640        650        660


               670
AE0155 TTGGAGTTACTGAAGAAA
          :::::: :::::::X :::
Seq1   TTGGAGCTACTGAATAAA
               670


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 100.0% identity in 10 nt overlap; init:   40, opt:   40


       50
AE0155 AGTTCAAGAA
       X::::::::X
Seq1   AGTTCAAGAA
       620


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